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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/924,400	08/07/2001	Tony N. Frudakis	210121.419C12	7385

500 7590 01/19/2006

SEED INTELLECTUAL PROPERTY LAW GROUP PLLC
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SUITE 6300
SEATTLE, WA 98104-7092

EXAMINER	
ZEMAN, MARY K	
ART UNIT	**PAPER NUMBER**
1631	

DATE MAILED: 01/19/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Interview Summary	Application No.	Applicant(s)	
	09/924,400	FRUDAKIS ET AL.	
	Examiner	Art Unit	
	Mary K. Zeman	1631	

All participants (applicant, applicant's representative, PTO personnel):

(1) *Mary K. Zeman (USPTO)*. (3)_____.

(2) *Julie Urvater (Appl Rep)*. (4)_____.

Date of Interview: *13 January 2006*.

Type: a)☒ Telephonic b)☐ Video Conference
c)☐ Personal [copy given to: 1)☐ applicant 2)☐ applicant's representative]

Exhibit shown or demonstration conducted: d)☐ Yes e)☒ No.
If Yes, brief description: _____.

Claim(s) discussed: *15 and 18*.

Identification of prior art discussed: *Frudakis 98/45328*.

Agreement with respect to the claims f)☐ was reached. g)☒ was not reached. h)☐ N/A.

Substance of Interview including description of the general nature of what was agreed to if an agreement was reached, or any other comments: *see attached*.

(A fuller description, if necessary, and a copy of the amendments which the examiner agreed would render the claims allowable, if available, must be attached. Also, where no copy of the amendments that would render the claims allowable is available, a summary thereof must be attached.)

THE FORMAL WRITTEN REPLY TO THE LAST OFFICE ACTION MUST INCLUDE THE SUBSTANCE OF THE INTERVIEW. (See MPEP Section 713.04). If a reply to the last Office action has already been filed, APPLICANT IS GIVEN A NON-EXTENDABLE PERIOD OF THE LONGER OF ONE MONTH OR THIRTY DAYS FROM THIS INTERVIEW DATE, OR THE MAILING DATE OF THIS INTERVIEW SUMMARY FORM, WHICHEVER IS LATER, TO FILE A STATEMENT OF THE SUBSTANCE OF THE INTERVIEW. See Summary of Record of Interview requirements on reverse side or on attached sheet.

See Attached

Examiner's signature, if required

Examiner Note: You must sign this form unless it is an Attachment to a signed Office action.

Summary of Record of Interview Requirements

Manual of Patent Examining Procedure (MPEP), Section 713.04, Substance of Interview Must be Made of Record
A complete written statement as to the substance of any face-to-face, video conference, or telephone interview with regard to an application must be made of record in the application whether or not an agreement with the examiner was reached at the interview.

Title 37 Code of Federal Regulations (CFR) § 1.133 Interviews
Paragraph (b)
In every instance where reconsideration is requested in view of an interview with an examiner, a complete written statement of the reasons presented at the interview as warranting favorable action must be filed by the applicant. An interview does not remove the necessity for reply to Office action as specified in §§ 1.111, 1.135. (35 U.S.C. 132)

37 CFR §1.2 Business to be transacted in writing.
All business with the Patent or Trademark Office should be transacted in writing. The personal attendance of applicants or their attorneys or agents at the Patent and Trademark Office is unnecessary. The action of the Patent and Trademark Office will be based exclusively on the written record in the Office. No attention will be paid to any alleged oral promise, stipulation, or understanding in relation to which there is disagreement or doubt.

The action of the Patent and Trademark Office cannot be based exclusively on the written record in the Office if that record is itself incomplete through the failure to record the substance of interviews.

It is the responsibility of the applicant or the attorney or agent to make the substance of an interview of record in the application file, unless the examiner indicates he or she will do so. It is the examiner's responsibility to see that such a record is made and to correct material inaccuracies which bear directly on the question of patentability.

Examiners must complete an Interview Summary Form for each interview held where a matter of substance has been discussed during the interview by checking the appropriate boxes and filling in the blanks. Discussions regarding only procedural matters, directed solely to restriction requirements for which interview recordation is otherwise provided for in Section 812.01 of the Manual of Patent Examining Procedure, or pointing out typographical errors or unreadable script in Office actions or the like, are excluded from the interview recordation procedures below. Where the substance of an interview is completely recorded in an Examiners Amendment, no separate Interview Summary Record is required.

The Interview Summary Form shall be given an appropriate Paper No., placed in the right hand portion of the file, and listed on the "Contents" section of the file wrapper. In a personal interview, a duplicate of the Form is given to the applicant (or attorney or agent) at the conclusion of the interview. In the case of a telephone or video-conference interview, the copy is mailed to the applicant's correspondence address either with or prior to the next official communication. If additional correspondence from the examiner is not likely before an allowance or if other circumstances dictate, the Form should be mailed promptly after the interview rather than with the next official communication.

The Form provides for recordation of the following information:
- Application Number (Series Code and Serial Number)
- Name of applicant
- Name of examiner
- Date of interview
- Type of interview (telephonic, video-conference, or personal)
- Name of participant(s) (applicant, attorney or agent, examiner, other PTO personnel, etc.)
- An indication whether or not an exhibit was shown or a demonstration conducted
- An identification of the specific prior art discussed
- An indication whether an agreement was reached and if so, a description of the general nature of the agreement (may be by attachment of a copy of amendments or claims agreed as being allowable). Note: Agreement as to allowability is tentative and does not restrict further action by the examiner to the contrary.
- The signature of the examiner who conducted the interview (if Form is not an attachment to a signed Office action)

It is desirable that the examiner orally remind the applicant of his or her obligation to record the substance of the interview of each case. It should be noted, however, that the Interview Summary Form will not normally be considered a complete and proper recordation of the interview unless it includes, or is supplemented by the applicant or the examiner to include, all of the applicable items required below concerning the substance of the interview.

A complete and proper recordation of the substance of any interview should include at least the following applicable items:
1) A brief description of the nature of any exhibit shown or any demonstration conducted,
2) an identification of the claims discussed,
3) an identification of the specific prior art discussed,
4) an identification of the principal proposed amendments of a substantive nature discussed, unless these are already described on the Interview Summary Form completed by the Examiner,
5) a brief identification of the general thrust of the principal arguments presented to the examiner,
   (The identification of arguments need not be lengthy or elaborate. A verbatim or highly detailed description of the arguments is not required. The identification of the arguments is sufficient if the general nature or thrust of the principal arguments made to the examiner can be understood in the context of the application file. Of course, the applicant may desire to emphasize and fully describe those arguments which he or she feels were or might be persuasive to the examiner.)
6) a general indication of any other pertinent matters discussed, and
7) if appropriate, the general results or outcome of the interview unless already described in the Interview Summary Form completed by the examiner.

Examiners are expected to carefully review the applicant's record of the substance of an interview. If the record is not complete and accurate, the examiner will give the applicant an extendable one month time period to correct the record.

Examiner to Check for Accuracy

If the claims are allowable for other reasons of record, the examiner should send a letter setting forth the examiner's version of the statement attributed to him or her. If the record is complete and accurate, the examiner should place the indication, "Interview Record OK" on the paper recording the substance of the interview along with the date and the examiner's initials.

Interview Summary, Attachment:
1/13/06

Issues regarding the rejections of record in this application were discussed. Potential claim language amendments to obviate the enablement rejection were discussed. Possible amendments to overcome the art and indefiniteness rejections were also discussed. Applicant was advised that amendments cannot introduce new matter. The examiner probed the file for the alignment of the claimed sequences with the applied prior art. In the IFW record, 11/8/02, in the Examiner Search Notes, the Examiner identified the original alignments relied upon. WO 98/45328 Frudakis et al, AAV68996, #188 shows approximately 300 contiguous nucleotides in common with SEQ ID NO: 302. In reviewing this file, the next sequence alignment was discovered: WO 98/45328 also discloses AAV68995, #187, which has approximately 650+ contiguous nucleotides in common with SEQ ID NO: 303.

Illustrative of the issues which may be applied again in the future with the oligonucleotide claim and the stretches of polyA in both sequences are the alignments of SEQ ID NO: 303 with AQ204617, AA533501, AQ063365, AI344928 and AI 344936. Each of these disclose short stretches of contiguous sequence in common with SEQ ID NO: 303.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Mary K Zeman whose telephone number is (571) 272 0723

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ardin Marschel, PhD can be reached on (571) 272 0718. The fax phone number for the organization where this application or proceeding is assigned is 571 273 8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of

the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

MARY K. ZEMAN
PRIMARY EXAMINER
AU 1631
1/13/06

```
Db    376 TCTGCTATGAAGACACTCAGGAGCAAGATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGC 435

Qy    214 TGCAGGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGGAGACCACGACGACTCTGCTATG 273

Db    436 TGCAGGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGGAGACCACGACGAYTCTGCTATG 495

Qy    274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGG 333

Db    496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGG 555

Qy    334 AGCGGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGGAGCCC 393

Db    556 AGCRGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGGAGCCC 615

Qy    394 AGGTACCACGTCCGTGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAA 453

Db    616 AGGTACCACGTCCGTGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAA 675

Qy    454 GTCCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGACGTGAACAAGAAGGACAAG 513

Db    676 GTCCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGACGTGAACAAGAAGGACAAG 735

Qy    514 CAAAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTC 573

Db    736 CAAAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTC 795

Qy    574 CTGCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGATA 633

Db    796 STGCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGAYA 855

Qy    634 AAGGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGAT 693

Db    856 AAGGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGAT 915

Qy    694 CCAAATATTCCAGATGAGTATGGAAATACCACTCT 728

Db    916 CCAAATATTCCAGATGAGTATGGAAATACCACTCT 950
```

RESULT 40
AAV68996
ID AAV68996 standard; DNA; 1853 BP.
XX
AC AAV68996;
XX
DT 22-JAN-1999 (first entry)
XX
DE DNA molecule encoding a breast tumour specific polypeptide #188.
XX
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
KW vaccine; epitope; endogenous; retroviral element; ss.
XX
OS Homo sapiens.
XX
PN WO9845328-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US06939.
XX
PR 11-DEC-1997; 97US-0991789.
PR 09-APR-1997; 97US-0838762.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM;
XX
DR WPI; 1998-557473/47.
XX
PT New DNA sequences isolated from endogenous human retroviral element
PT - and related vectors, transformed cells, proteins and antibodies,
PT useful for diagnosis, treatment and prevention of breast cancer
XX
PS Claim 1; Page 138-139; 173pp; English.
XX
CC AAV68800 to AAV68998 represent nucleotide sequences which encode human
CC breast tumour specific polypeptides. Detection or measurement of
CC human breast tumour specific polypeptides and nucleotide sequences,
CC or the corresponding RNA in a sample, is used for diagnosis and
CC monitoring of breast cancer. Human breast tumour specific polypeptides
CC and nucleotide sequences, and the vectors containing the DNAs, are also
CC useful in vaccines for inhibiting development (for prevention or
CC therapy) of breast cancer. The polypeptides may also be used to
CC raise monoclonal antibodies, used as immunoassay reagents.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.4%; Score 252; DB 19; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     34 TCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGC 93

Db    256 TCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGC 315

Qy     94 TTCCCCTGCTGCAGGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACGACGAC 153

Db    316 TTCCCCTGCTGCAGGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACGACGAC 375

Qy    154 TCTGCTATGAAGACACTCAGGAGCAAGATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGC 213

Db    376 TCTGCTATGAAGACACTCAGGAGCAAGATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGC 435

Qy    214 TGCAGGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGGAGACCACGACGACTCTGCTATG 273

Db    436 TGCAGGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGGAGACCACGACGAYTCTGCTATG 495

Qy    274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGG 333

Db    496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGG 555

Qy    334 AGC 336

Db    556 AGC 558
```

RESULT 41
AAC81007
ID AAC81007 standard; cDNA; 1853 BP.
XX
AC AAC81007;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human B11Ag1 antigen protein coding exon cDNA SEQ ID NO: 295.
XX
KW Human; breast tumour-specific antigen; cytostatic; vaccine;
KW breast cancer; B18Ag1; B11Ag1; B15Ag1; ss.
XX
OS Homo sapiens.
XX
PN WO200061753-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US09312.
XX
PR 09-APR-1999; 99US-0289198.
PR 28-OCT-1999; 99US-0429755.
PR 23-MAR-2000; 2000US-0534825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX

```
OS   Homo sapiens.
XX
PN   WO200190152-A2.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16776.
XX
PR   24-MAY-2000; 2000US-0577505.
PR   08-JUN-2000; 2000US-0590583.
PR   26-OCT-2000; 2000US-0699295.
PR   16-MAR-2001; 2001US-0810936.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Frudakis TN,  Reed SG,  Smith JM,  Misher LE,  Dillon DC,  Retter MW;
PI   Wang A,  Skeiky YAW,  Harlocker SL,  Day CH;
XX
DR   WPI; 2002-089919/12.
DR   P-PSDB; AAU74390.
XX
PT   New breast tumour proteins and polynucleotides encoding them, useful for
PT   treating and/or preventing cancer, particularly breast cancer, and for
PT   eliciting humoral and/or cellular immune response -
XX
PS   Claim 1; Page 239; 245pp; English.
XX
CC   The invention relates to novel breast tumour polynucleotides and
CC   polypeptides. The polypeptides and polynucleotides are useful in
CC   pharmaceutical compositions for treating and/or preventing cancer,
CC   particularly breast cancer, and for eliciting an immune response,
CC   particularly humoral and/or cellular immune response. The polynucleotides
CC   may be used as probes or primers for nucleic acid hybridisation, in the
CC   design and preparation of ribozyme molecules for inhibiting expression of
CC   tumour polypeptides and proteins, and in recombinant DNA molecules to
CC   direct expression of a polypeptide in host cells. AAS99570-AAS99888
CC   represent novel human breast cancer protein coding sequences and
CC   PCR primers of the invention.
XX
SQ   Sequence 1155 BP; 346 A; 253 C; 296 G; 260 T; 0 other;

  Query Match             47.8%;  Score 975;  DB 24;  Length 1155;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1125;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 ATGGTGGTTGAGGTTGATTCCATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTTGGTCTC 60
Db       1 ATGGTGGTTGAGGTTGATTCCATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTTGGTCTC 60

Qy      61 AGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGCTTCCCCTGCTGCAGGGAGAGCGGCAAG 120
Db      61 AGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGCTTCCCCTGCTGCAGGGAGAGCGGCAAG 120

Qy     121 AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGCTATGAAGACACTCAGGAGCAAG 180
Db     121 AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGCTATGAAGACACTCAGGAGCAAG 180

Qy     181 ATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGCTGCAGGGGGAGTGGCAAGAGCAACGTG 240
Db     181 ATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGCTGCAGGGGGAGTGGCAAGAGCAACGTG 240

Qy     241 GGCGCTTCTGGAGACCACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300
Db     241 GGCGCTTCTGGAGACCACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300

Qy     301 TGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGGAGCGGCAAGAGCAAGGTGGGCGCTTGG 360
Db     301 TGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGGAGCAGCAAGAGCAAGGTGGGCGCTTGG 360

Qy     361 GGAGACTACGATGACAGTGCCTTCATGGAGCCCAGGTACCACGTCCGTGGAGAAGATCTG 420
Db     361 GGAGACTACGATGACAGTGCCTTCATGGAGCCCAGGTACCACGTCCGTGGAGAAGATCTG 420

Qy     421 GACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGTCCCCAGAAAGGATCTCATCGTCATG 480
Db     421 GACAAGCTCCACAGAGCTGCCTGGTGGGGTAAAGTCCCCAGAAAGGATCTCATCGTCATG 480

Qy     481 CTCAGGGACACTGACGTGAACAAGAAGGACAAGCAAAAGAGGACTGCTCTACATCTGGCC 540
Db     481 CTCAGGGACACTGACGTGAACAAGCAGGACAAGCAAAAGAGGACTGCTCTACATCTGGCC 540

Qy     541 TCTGCCAATGGGAATTCAGAAGTAGTAAAACTCCTGCTGGACAGACGATGTCAACTTAAT 600
Db     541 TCTGCCAATGGGAATTCAGAAGTAGTAAAACTCCTGCTGGACAGACGATGTCAACTTAAT 600

Qy     601 GTCCTTGACAACAAAAAGAGGACAGCTCTGATAAAGGCCGTACAATGCCAGGAAGATGAA 660
Db     601 GTCCTTGACAACAAAAAGAGGACAGCTCTGATAAAGGCCGTACAATGCCAGGAAGATGAA 660

Qy     661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATGAGTATGGAAAT 720
Db     661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATGAGTATGGAAAT 720

Qy     721 ACCACTCTGCACTACGCTATCTATAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA 780
Db     721 ACCACTCTGCACTACGCTATCTATAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA 780

Qy     781 TATGGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTGTTACTTGGTGTA 840
Db     781 TATGGTGCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACTGTTACTTGGTGTA 840

Qy     841 CATGAGCAAAAACAGCAAGTCGTGAAATTTTTAATCAAGAAAAAAGCGAATTTAAATGCA 900
Db     841 CATGAGCAAAAACAGCAAGTCGTGAAATTTTTAATTAAGAAAAAAGCGAATTTAAATGCA 900

Qy     901 CTGGATAGATATGGAAGGACTGCTCTCATACTTGCTGTATGTTGTGGATCAGCAAGTATA 960
Db     901 CTGGATAGATATGGAAGGACTGCTCTCATACTTGCTGTATGTTGTGGATCAGCAAGTATA 960

Qy     961 GTCAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGACG 1020
Db     961 GTCAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGACG 1020

Qy    1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db    1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

Qy    1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAA 1128
Db    1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAA 1128

RESULT 30
AAV68995
ID   AAV68995 standard; DNA; 1512 BP.
XX
AC   AAV68995;
XX
DT   22-JAN-1999  (first entry)
XX
DE   DNA molecule encoding a breast tumour specific polypeptide #187.
XX
KW   Human; breast cancer; breast tumour tissue; diagnosis; treatment;
KW   vaccine; epitope; endogenous; retroviral element; ss.
XX
OS   Homo sapiens.
XX
PN   WO9845328-A2.
XX
PD   15-OCT-1998.
XX
PF   09-APR-1998;   98WO-US06939.
XX
PR   11-DEC-1997;   97US-0991789.
PR   09-APR-1997;   97US-0838762.
XX
```

INT SUMMARY

```
PA   (CORI-) CORIXA CORP.
XX
PI   Frudakis TN,  Reed SG,  Smith JM;
XX
DR   WPI; 1998-557473/47.
XX
PT   New DNA sequences isolated from endogenous human retroviral element
PT   - and related vectors, transformed cells, proteins and antibodies,
PT   useful for diagnosis, treatment and prevention of breast cancer
XX
PS   Claim 1; Page 137-138; 173pp; English.
XX
CC   AAV68800 to AAV68998 represent nucleotide sequences which encode human
CC   breast tumour specific polypeptides. Detection or measurement of
CC   human breast tumour specific polypeptides and nucleotide sequences,
CC   or the corresponding RNA in a sample, is used for diagnosis and
CC   monitoring of breast cancer. Human breast tumour specific polypeptides
CC   and nucleotide sequences, and the vectors containing the DNAs, are also
CC   useful in vaccines for inhibiting development (for prevention or
CC   therapy) of breast cancer. The polypeptides may also be used to
CC   raise monoclonal antibodies, used as immunoassay reagents.
XX
SQ   Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

  Query Match             24.1%;  Score 491;  DB 19;  Length 1512;
  Best Local Similarity   99.4%;  Pred. No. 6.4e-180;
  Matches  691;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      34 TCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGC 93
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 TCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGC 315

Qy      94 TTCCCCTGCTGCAGGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACGACGAC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 TTCCCCTGCTGCAGGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACGACGAC 375

Qy     154 TCTGCTATGAAGACACTCAGGAGCAAGATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGC 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 TCTGCTATGAAGACACTCAGGAGCAAGATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGC 435

Qy     214 TGCAGGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGGAGACCACGACGACTCTGCTATG 273
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     436 TGCAGGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGGAGACCACGACGAYTCTGCTATG 495

Qy     274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGG 333
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGCTGCCACTGCTTCCCCTGCTGCAGGGGG 555

Qy     334 AGCGGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGGAGCCC 393
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     556 AGCRGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGGAGCCC 615

Qy     394 AGGTACCACGTCCGTGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAA 453
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     616 AGGTACCACGTCCGTGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGGTAAA 675

Qy     454 GTCCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGACGTGAACAAGAAGGACAAG 513
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 GTCCCCAGAAAGGATCTCATCGTCATGCTCAGGGACACTGACGTGAACAAGAAGGACAAG 735

Qy     514 CAAAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTC 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     736 CAAAAGAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAAGTAGTAAAACTC 795

Qy     574 CTGCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGATA 633
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     796 STGCTGGACAGACGATGTCAACTTAATGTCCTTGACAACAAAAAGAGGACAGCTCTGAYA 855

Qy     634 AAGGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGAT 693
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     856 AAGGCCGTACAATGCCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCACTGAT 915

Qy     694 CCAAATATTCCAGATGAGTATGGAAATACCACTCT 728
           |||||||||||||||||||||||||||||||||||
Db     916 CCAAATATTCCAGATGAGTATGGAAATACCACTCT 950


RESULT 31
AAC81006
ID   AAC81006 standard; cDNA; 1512 BP.
XX
AC   AAC81006;
XX
DT   13-FEB-2001  (first entry)
XX
DE   Human B11Ag1 antigen protein coding exon cDNA SEQ ID NO: 294.
XX
KW   Human; breast tumour-specific antigen; cytostatic; vaccine;
KW   breast cancer; B18Ag1; B11Ag1; B15Ag1; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061753-A2.
XX
PD   19-OCT-2000.
XX
PF   07-APR-2000; 2000WO-US09312.
XX
PR   09-APR-1999;   99US-0289198.
PR   28-OCT-1999;   99US-0429755.
PR   23-MAR-2000; 2000US-0534825.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Frudakis TN,  Smith JM,  Reed SG,  Misher LE,  Retter MW,  Dillon DC;
XX
DR   WPI; 2000-628403/60.
XX
PT   An isolated polypeptide comprising an immunogenic portion of a breast
PT   tumor protein used for inhibiting the development of cancer, especially
PT   breast cancer, and monitoring cancer progression in a patient -
XX
PS   Claim 4; Page 172; 187pp; English.
XX
CC   The present sequence is given in a specification relating to compositions
CC   and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC   sequences that are preferentially expressed in breast tumour tissue, and
CC   the polypeptides encoded by such nucleotide sequences, are used in
CC   compositions and vaccines to inhibit the development of cancer,
CC   especially breast cancer. The progression of a cancer may be monitored by
CC   carrying out detection of tumour-specific antigens at subsequent time
CC   points and comparing the results from the different time points.
CC   CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC   with tumour-specific polypeptides, polynucleotides encoding the
CC   polypeptides or antigen presenting cells expressing the polypeptides. The
CC   cells are then administered to the patient to inhibit development of
CC   cancer.
XX
SQ   Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

  Query Match             24.1%;  Score 491;  DB 21;  Length 1512;
  Best Local Similarity   99.4%;  Pred. No. 6.4e-180;
  Matches  691;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      34 TCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGC 93
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 TCTTCTGTGAAGAAGCCATTTGGTCTCAGGAGCAAGATGGGCAAGTGGTGCTGCCGTTGC 315

Qy      94 TTCCCCTGCTGCAGGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACGACGAC 153
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 TTCCCCTGCTGCAGGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGGAGACCACGACGAC 375

Qy     154 TCTGCTATGAAGACACTCAGGAGCAAGATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGC 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 TCTGCTATGAAGACACTCAGGAGCAAGATGGGCAAGTGGTGCCGCCACTGCTTCCCCTGC 435
```

(13) INT. SUM MARY

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 08:45:54 ; Search time 2565.15 Seconds
(without alignments)
12879.875 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atggtggttgaggttgattc.....aaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1430706

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	184	9.0	521	17	AQ204617	AQ204617 HS_3229_B
2	141	6.9	865	12	BF676987	BF676987 602084215
3	140	6.9	451	9	AI804733	AI804733 tu42b03.x
4	137	6.7	289	9	AA533501	AA533501 nj96a04.s
5	129	6.3	531	17	AQ615477	AQ615477 HS_5144_B
6	117	5.7	621	14	BM763942	BM763942 K-EST0045
7	117	5.7	633	14	BM763453	BM763453 K-EST0044
8	117	5.7	817	14	BQ441373	BQ441373 AGENCOURT
9	89	4.4	400	17	AQ124119	AQ124119 HS_3122_A
c 10	87	4.3	399	17	AQ030111	AQ030111 RPCI11-39
11	87	4.3	544	9	AL703938	AL703938 DKFZp686E
c 12	79	3.9	279	13	BI461255	BI461255 603206584
13	73	3.6	385	17	AQ063365	AQ063365 CIT-HSP-2
c 14	59	2.9	707	17	AG045796	AG045796 Pan trogl
c 15	57	2.8	607	17	B48260	B48260 RPCI11-6K4.
c 16	52	2.5	380	12	BF329652	BF329652 RC6-BN027
17	50	2.5	592	17	AQ372700	AQ372700 RPCI11-14
c 18	49	2.4	495	17	AQ469831	AQ469831 CITBI-E1-
c 19	49	2.4	557	17	AQ469663	AQ469663 CITBI-E1-
c 20	49	2.4	667	17	AG156382	AG156382 Pan trogl
c 21	49	2.4	697	17	AQ030113	AQ030113 RPCI11-39
22	47	2.3	187	10	BE069869	BE069869 CM1-BT039
c 23	47	2.3	476	17	AQ392059	AQ392059 CITBI-E1-
24	46	2.3	400	17	AQ057106	AQ057106 CIT-HSP-2
25	45	2.2	894	12	BF675049	BF675049 602136643
26	44	2.2	460	17	AQ360298	AQ360298 HS_5035_A
27	41	2.0	710	17	AG165908	AG165908 Pan trogl
c 28	40	2.0	503	17	B55862	B55862 CIT-HSP-200
29	39	1.9	1011	17	AQ900910	AQ900910 HS_2055_B
30	38	1.9	458	17	AQ247090	AQ247090 HS_2055_B
c 31	37	1.8	424	17	AQ763344	AQ763344 HS_3162_A
32	37	1.8	694	12	BG720647	BG720647 602692528
33	36	1.8	652	17	AG054405	AG054405 Pan trogl
34	35	1.7	156	9	AI349163	AI349163 ta73c06.x
35	35	1.7	157	9	AI251211	AI251211 qv38h06.x
36	35	1.7	160	9	AI305627	AI305627 qw72f03.x
37	35	1.7	166	9	AI343314	AI343314 tb93g12.x
38	35	1.7	184	10	AW302924	AW302924 xr86g07.x
39	35	1.7	199	10	AW302925	AW302925 xr86g08.x
40	35	1.7	224	9	AI344928	AI344928 tb01a04.x
41	35	1.7	232	9	AI336592	AI336592 ta94d12.x
42	35	1.7	239	9	AI344933	AI344933 tb01a11.x
43	35	1.7	239	9	AI344936	AI344936 tb01b03.x
44	35	1.7	250	9	AI335449	AI335449 tb79f03.x
c 45	35	1.7	360	9	AI494279	AI494279 qy98c11.x

ALIGNMENTS

RESULT 1
AQ204617
LOCUS AQ204617 521 bp DNA linear GSS 17-SEP-1998
DEFINITION HS_3229_B1_G12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=23 Row=N, DNA sequence.
ACCESSION AQ204617
VERSION AQ204617.1 GI:3615187
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Purlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 row: N column: 23

```
           Class: BAC ends
           High quality sequence stop: 521.
FEATURES             Location/Qualifiers
     source          1. .521
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=3229 Col=23 Row=N"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT      161 a     94 c     99 g    161 t     6 others
ORIGIN

  Query Match             9.0%;  Score 184;  DB 17;  Length 521;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-35;
  Matches  184;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1595 AGCTAGAAAATTTTATGGCTATCGAAGAAATGAAGAAGCACGGAAGTACTCATGTCGGAT 1654
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     231 AGCTAGAAAATTTTATGGCTATCGAAGAAATGAAGAAGCACGGAAGTACTCATGTCGGAT 290

Qy    1655 TCCCAGAAAACCTGACTAATGGTGCCACTGCTGGCAATGGTGATGATGGATTAATTCCTC 1714
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     291 TCCCAGAAAACCTGACTAATGGTGCCACTGCTGGCAATGGTGATGATGGATTAATTCCTC 350

Qy    1715 CAAGGAAGAGCAGAACACCTGAAAGCCAGCAATTTCCTGACACTGAGAATGAAGAGTATC 1774
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     351 CAAGGAAGAGCAGAACACCTGAAAGCCAGCAATTTCCTGACACTGAGAATGAAGAGTATC 410

Qy    1775 ACAG 1778
           ||||
Db     411 ACAG 414


RESULT 2
BF676987
LOCUS       BF676987                865 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602084215F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248746 5',
            mRNA sequence.
ACCESSION   BF676987
VERSION     BF676987.1  GI:11950882
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 865)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1067  row: m  column: 03
            High quality sequence stop: 642.
FEATURES             Location/Qualifiers
     source          1. .865
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4248746"
                     /clone_lib="NIH_MGC_83"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc
                     ); 5' and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).   Average
                     insert size 1.4 kb (range 0.5-4.0 kb).  14/15 colonies
                     contained inserts  by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA)."
BASE COUNT      297 a    140 c    211 g    217 t
ORIGIN

  Query Match             6.9%;  Score 141;  DB 12;  Length 865;
  Best Local Similarity   100.0%;  Pred. No. 2e-25;
  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     919 ACTGCTCTCATACTTGCTGTATGTTGTGGATCAGCAAGTATAGTCAGCCTTCTACTTGAG 978
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 ACTGCTCTCATACTTGCTGTATGTTGTGGATCAGCAAGTATAGTCAGCCTTCTACTTGAG 412

Qy     979 CAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGACGGCCAGAGAGTATGCTGTT 1038
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 CAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGACGGCCAGAGAGTATGCTGTT 472

Qy    1039 TCTAGTCATCATCATGTAATT 1059
           |||||||||||||||||||||
Db     473 TCTAGTCATCATCATGTAATT 493


RESULT 3
AI804733
LOCUS       AI804733                451 bp    mRNA    linear   EST 03-MAR-2000
DEFINITION  tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253677 3',
            mRNA sequence.
ACCESSION   AI804733
VERSION     AI804733.1  GI:5370205
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 543  Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2253677"
                     /clone_lib="NCI_CGAP_Pr28"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.
```

Int. Summary (5)

```
BASE COUNT      128 a     79 c     91 g    153 t
ORIGIN

  Query Match             6.9%;  Score 140;  DB 9;  Length 451;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-25;
  Matches  140;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     916 AGGACTGCTCTCATACTTGCTGTATGTTGTGGATCAGCAAGTATAGTCAGCCTTCTACTT 975
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47 AGGACTGCTCTCATACTTGCTGTATGTTGTGGATCAGCAAGTATAGTCAGCCTTCTACTT 106

Qy     976 GAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGACGGCCAGAGAGTATGCT 1035
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107 GAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGACGGCCAGAGAGTATGCT 166

Qy    1036 GTTTCTAGTCATCATCATGT 1055
           ||||||||||||||||||||
Db     167 GTTTCTAGTCATCATCATGT 186


RESULT 4
AA533501
LOCUS       AA533501                 289 bp    mRNA    linear   EST 21-AUG-1997
DEFINITION  nj96a04.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000302,
            mRNA sequence.
ACCESSION   AA533501
VERSION     AA533501.1  GI:2277597
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 289)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
            Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 217   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .289
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1000302"
                     /clone_lib="NCI_CGAP_Pr11"
                     /sex="male"
                     /tissue_type="normal prostatic epithelial cells"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pAMP10; mRNA made from
                     normal prostatic epithelial cells, cDNA made by oligo-dT
                     priming.  Non-directionally cloned.  Size-selected on
                     agarose gel, average insert size 600 bp.  Library made by
                     D. Krizman, NIH."
BASE COUNT      121 a     36 c     66 g     66 t
ORIGIN

  Query Match             6.7%;  Score 137;  DB 9;  Length 289;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-24;
  Matches  137;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1788 AAATGATACTCAGAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACACGATGAGAT 1847
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 AAATGATACTCAGAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACACGATGAGAT 68

Qy    1848 TCTGATTCATGAAGAAAAGCAGATAGAAGTGGTTGAAAAAATGAATTCTGAGCTTTCTCT 1907
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 TCTGATTCATGAAGAAAAGCAGATAGAAGTGGTTGAAAAAATGAATTCTGAGCTTTCTCT 128

Qy    1908 TAGTTGTAAGAAAGAAA 1924
           |||||||||||||||||
Db     129 TAGTTGTAAGAAAGAAA 145


RESULT 5
AQ615477
LOCUS       AQ615477                 531 bp    DNA     linear   GSS 15-JUN-1999
DEFINITION  HS_5144_B1_G01_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=720 Col=1 Row=N, DNA sequence.
ACCESSION   AQ615477
VERSION     AQ615477.1  GI:5076753
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 720  row: N  column: 1
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 531.
FEATURES             Location/Qualifiers
     source          1. .531
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=720 Col=1 Row=N"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
BASE COUNT      167 a     92 c     92 g    169 t     11 others
ORIGIN

  Query Match             6.3%;  Score 129;  DB 17;  Length 531;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-22;
  Matches  129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     682 CATGGCACTGATCCAAATATTCCAGATGAGTATGGAAATACCACTCTGCACTACGCTATC 741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     117 CATGGCACTGATCCAAATATTCCAGATGAGTATGGAAATACCACTCTGCACTACGCTATC 176

Qy     742 TATAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTATATGGTGCTGATATCGAATCA 801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     177 TATAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTATATGGTGCTGATATCGAATCA 236
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© INT. SUMMARY

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  Query Match             3.9%;  Score 79;  DB 13;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-10;
  Matches   79;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ATGGTGGTTGAGGTTGATTCCATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTTGGTCTC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      84 ATGGTGGTTGAGGTTGATTCCATGCCGGCTGCCTCTTCTGTGAAGAAGCCATTTGGTCTC 25

Qy      61 AGGAGCAAGATGGGCAAGT 79
           ||||||||||||||||||||
Db      24 AGGAGCAAGATGGGCAAGT 6


RESULT 13
AQ063365
LOCUS       AQ063365                385 bp    DNA     linear   GSS 31-JUL-1998
DEFINITION  CIT-HSP-2348P17.TR CIT-HSP Homo sapiens genomic clone 2348P17, DNA
            sequence.
ACCESSION   AQ063365
VERSION     AQ063365.1  GI:3361196
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 385)
  AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
            Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
            Simon,M. and Venter,J.C.
  TITLE     Use of a random BAC End Sequence Database for Sequence-Ready Map
            Building (1998)
  JOURNAL   Unpublished (1998)
COMMENT     Other_GSSs: CIT-HSP-2348P17.TF
            Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .385
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2348P17"
                     /clone_lib="CIT-HSP"
                     /sex="Male"
                     /cell_type="Sperm"
                     /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                     HindIII"
BASE COUNT      118 a     53 c     79 g    135 t
ORIGIN

  Query Match             3.6%;  Score 73;  DB 17;  Length 385;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   73;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1408 AGAATTTGCGAATTAGTTTCTGACTACAAAGAAAAACAGATGCCAAAATACTCTTCTGAA 1467
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     189 AGAATTTGCGAATTAGTTTCTGACTACAAAGAAAAACAGATGCCAAAATACTCTTCTGAA 248

Qy    1468 AACAGCAACCCAG 1480
           |||||||||||||
Db     249 AACAGCAACCCAG 261


RESULT 14
AG045796/c
LOCUS       AG045796                707 bp    DNA     linear   GSS 02-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-024N04.R, genomic survey sequence.
ACCESSION   AG045796
VERSION     AG045796.1  GI:16582688
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
            BAC Library clone:PTB-024N04.R.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 707)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .707
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB-024N04.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      233 a    145 c     85 g    217 t      7 others
ORIGIN

  Query Match             2.9%;  Score 59;  DB 17;  Length 707;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-05;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1956 GGAAGAAATTGCCATGCTAAGACTGGAGCTAGACACAATGAAACATCAGAGCCAGCTAA 2014
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     226 GGAAGAAATTGCCATGCTAAGACTGGAGCTAGACACAATGAAACATCAGAGCCAGCTAA 168


RESULT 15
B48260/c
LOCUS       B48260                  607 bp    DNA     linear   GSS 08-APR-1999
DEFINITION  RPCI11-6K4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6K4, DNA
            sequence.
ACCESSION   B48260
VERSION     B48260.1  GI:2600497
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 607)
  AUTHORS   Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
            ,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences for Sequence-Ready Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Mark Adams
```

Int Summary D

```
          Email: cgapbs-r@mail.nih.gov
          cDNA Library Preparation: David B. Krizman, Ph.D.
           cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .199
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2767070"
                     /clone_lib="NCI_CGAP_Lu26"
                     /tissue_type="invasive adenocarcinoma"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pAMP1; mRNA made from lung
                     adenocarcinoma tissue, cDNA made by oligo-dT  priming.
                     Directionally cloned.  Size-selected on agarose  gel,
                     average insert size 500 bp.  Primary library,
                     non-amplified.  "
BASE COUNT       93 a      38 c      40 g      28 t
ORIGIN

  Query Match             1.7%;  Score 35;  DB 10;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
           ||||||||||||||||||||||||||||||||||||
Db     111 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 145


RESULT 40
AI344928
LOCUS       AI344928               224 bp    mRNA    linear   EST 30-DEC-1998
DEFINITION  tb01a04.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052270 3',
            mRNA sequence.
ACCESSION   AI344928
VERSION     AI344928.1  GI:4082134
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 224)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .224
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2052270"
                     /clone_lib="NCI_CGAP_Lu26"
                     /tissue_type="invasive adenocarcinoma"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pAMP1; mRNA made from lung
                     adenocarcinoma tissue, cDNA made by oligo-dT  priming.
                     Directionally cloned.  Size-selected on agarose  gel,
                     average insert size 500 bp.  Primary library,
                     non-amplified.  "
BASE COUNT       119 a      40 c      36 g      29 t
ORIGIN

  Query Match             1.7%;  Score 35;  DB 9;  Length 224;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
           ||||||||||||||||||||||||||||||||||||
Db     128 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 162


RESULT 41
AI336592
LOCUS       AI336592               232 bp    mRNA    linear   EST 16-FEB-1999
DEFINITION  ta94d12.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2051735 3',
            mRNA sequence.
ACCESSION   AI336592
VERSION     AI336592.1  GI:4073519
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 232)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 302   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 225.
FEATURES             Location/Qualifiers
     source          1. .232
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2051735"
                     /clone_lib="NCI_CGAP_Lu26"
                     /tissue_type="invasive adenocarcinoma"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pAMP1; mRNA made from lung
                     adenocarcinoma tissue, cDNA made by oligo-dT  priming.
                     Directionally cloned.  Size-selected on agarose  gel,
                     average insert size 500 bp.  Primary library,
                     non-amplified.  "
BASE COUNT       119 a      44 c      40 g      29 t
ORIGIN

  Query Match             1.7%;  Score 35;  DB 9;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
           ||||||||||||||||||||||||||||||||||||
Db     134 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 168


RESULT 42
AI344933
LOCUS       AI344933               239 bp    mRNA    linear   EST 16-FEB-1999
DEFINITION  tb01a11.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052284 3',
            mRNA sequence.
ACCESSION   AI344933
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Int. Summary

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VERSION     AI344933.1  GI:4082139
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 239)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 291   Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .239
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2052284"
                     /clone_lib="NCI_CGAP_Lu26"
                     /tissue_type="invasive adenocarcinoma"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pAMP1; mRNA made from lung
                     adenocarcinoma tissue, cDNA made by oligo-dT  priming.
                     Directionally cloned.  Size-selected on agarose  gel,
                     average insert size 500 bp.  Primary library,
                     non-amplified.  "
BASE COUNT      119 a     48 c     40 g     32 t
ORIGIN

  Query Match             1.7%;  Score 35;  DB 9;  Length 239;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
           ||||||||||||||||||||||||||||||||||||
Db     146 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 180


RESULT 43
AI344936
LOCUS       AI344936                239 bp    mRNA    linear   EST 30-DEC-1998
DEFINITION  tb01b03.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052269 3',
            mRNA sequence.
ACCESSION   AI344936
VERSION     AI344936.1  GI:4082142
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 239)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .239
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2052269"
                     /clone_lib="NCI_CGAP_Lu26"
                     /tissue_type="invasive adenocarcinoma"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pAMP1; mRNA made from lung
                     adenocarcinoma tissue, cDNA made by oligo-dT  priming.
                     Directionally cloned.  Size-selected on agarose  gel,
                     average insert size 500 bp.  Primary library,
                     non-amplified.  "
BASE COUNT      119 a     48 c     40 g     32 t
ORIGIN

  Query Match             1.7%;  Score 35;  DB 9;  Length 239;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
           ||||||||||||||||||||||||||||||||||||
Db     146 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 180


RESULT 44
AI335449
LOCUS       AI335449                250 bp    mRNA    linear   EST 29-DEC-1998
DEFINITION  tb79f03.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2060573 3',
            mRNA sequence.
ACCESSION   AI335449
VERSION     AI335449.1  GI:4072376
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
             cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            High quality sequence stop: 240.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2060573"
                     /clone_lib="NCI_CGAP_Lu26"
                     /tissue_type="invasive adenocarcinoma"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: lung; Vector: pAMP1; mRNA made from lung
                     adenocarcinoma tissue, cDNA made by oligo-dT  priming.
                     Directionally cloned.  Size-selected on agarose  gel,
                     average insert size 500 bp.  Primary library,
                     non-amplified.  "
BASE COUNT      136 a     43 c     41 g     30 t
ORIGIN

  Query Match             1.7%;  Score 35;  DB 9;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

Int Summary